

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 08:42:15 ; Search time 20.5 Seconds
(without alignments)
117.237 Million cell updates/sec

Title: US-09-913-524-9

Perfect score: 143

Sequence: 1 PWSPAALLRLQRPPEPSAHAFCHR 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR73:*

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	143	100.0	366	1 A40056	inhibin alpha chain
2	140	97.9	366	1 JC1106	inhibin alpha chain
3	131	91.6	360	1 A25732	inhibin alpha chain
4	128	89.5	366	1 A24248	inhibin alpha chain
5	127	88.8	364	1 WPPCA	inhibin alpha chain
6	89	62.2	328	2 F51215	inhibin alpha-subu
7	54	37.8	2504	1 A57788	enoyl-facyl-carrie
8	51	35.7	451	1 UBHUG	tubulin gamma chain
9	51	35.7	451	1 UBXLG	tubulin gamma chain
10	49	34.3	365	2 E83800	hypothetical prote
11	48	33.6	128	2 T44497	hypothetical prote
12	48	33.6	192	2 T09436	hypothetical prote
13	48	33.6	192	2 JC4207	nifz protein - Fra
14	47	32.9	102	2 A49361	nitrogenase Nifz c
15	47	32.9	181	2 H87577	peripheral benzod
16	47	32.9	528	2 S35272	nitroreductase fam
17	47	32.9	577	2 T14315	dihydrofolate redu
18	47	32.9	679	2 T19703	hypothetical prote
19	47	32.9	2302	2 T14328	protein-tyrosine-p
20	47	32.9	2509	2 G01880	fatty-acid synthas
21	46.5	32.5	257	2 AH2839	conserved hypothet
22	46.5	32.5	257	2 B97617	similar to orr3 ge
23	46.5	32.5	391	2 S68354	heme d1 synthetas
24	46.5	32.5	428	2 F81660	histidyl-tRNA synt
25	46.5	32.5	576	2 G96763	probable MAP kinas
26	46	32.2	123	2 D87587	hypothetical prote
27	46	32.2	297	1 YXUNTP	thymidylate syntha
28	46	32.2	351	2 S58192	hypothetical prote
29	46	32.2	430	2 T36892	hypothetical prote

30	46	32.2	468	2 T50873	hypothetical prote
31	46	32.2	483	2 A3425	xylulokinase (EC 2
32	46	32.2	630	2 A36359	VSG expression sit
33	46	32.2	1844	1 RRPWTM	genome polypeptid
34	46	32.2	1844	2 S01956	hypothetical prote
35	46	32.2	1914	2 T42635	tenascin Y precurs
36	46	32.2	1985	2 S19151	hypothetical prote
37	45.5	31.8	323	2 S62085	hrpW protein - Pse
38	45.5	31.8	398	2 J01245	hypothetical 43K p
39	45.5	31.8	516	2 H84424	probable MAP kinas
40	45.5	31.8	824	2 B47301	VirB4 homolog - Bo
41	45.5	31.8	3988	1 GNRVBY	genome polypeptid
42	45	31.5	63	2 I52277	platelet-derived g
43	45	31.5	204	2 A55671	bad protein - mous
44	45	31.5	356	2 E83591	hypothetical prote
45	45	31.5	404	2 S42578	gene prune protein

ALIGNMENTS

RESULT 1
A40056
inhibin alpha chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 08-Dec-2000
C:Accession: A41398; A40056; A40905
R:Feng, Z.M.; Li, Y.P.; Chen, C.L.C.
Mol. Endocrinol. 3, 1914-1925, 1989
A:Title: Analysis of the 5'-flanking regions of rat inhibin alpha- and beta-B-subun.
A:Reference number: A41398; MUID:90190649; PMID:2628729
A:Accession: A41398
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-366 <FEN>
A:Cross-references: GB:M32754; GB:M32755; NID:g204939; PIDN:AAA41437.1; PID:g204941
R:Woodruff, T.K.; Meunier, H.; Jones, P.B.C.; Hsueh, A.J.W.; Mayo, K.E.
Mol. Endocrinol. 1, 561-568, 1987
A:Title: Rat inhibin: molecular cloning of alpha- and beta-subunit complementary dea
A:Reference number: A40056; MUID:91042598; PMID:3153478
A:Accession: A40056
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-366 <MOO>
A:Cross-references: GB:M36453; NID:g204934; PIDN:AAA41435.1; PID:g204935
R:Esch, F.S.; Shimasaki, S.; Cooksey, K.; Mercado, M.; Mason, A.J.; Ying, S.Y.; Uenk
Mol. Endocrinol. 1, 388-396, 1987
A:Title: Complementary deoxyribonucleic acid (cDNA) cloning and DNA sequence analys
A:Reference number: A40905; MUID:90331931; PMID:2484214
A:Accession: A40905
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-366 <ESC>
A:Suprafamily: inhibin
C:Keywords: glycoprotein
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-233/Domain: propeptide #status predicted <PRO>
F:234-366/Product: inhibin alpha chain #status predicted <MAT>
F:147,269/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 143; DB 1; Length 366;
Best Local Similarity 100.0%; Pred. No. 8.3e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PWSPAALLRLQRPPEPSAHAFCHR 25
|||||
DB 241 PWSPAALLRLQRPPEPSAHAFCHR 265

RESULT 2
JC1106
inhibin alpha chain precursor - mouse
C:Species: Mus musculus (house mouse)

C>Date: 10-Sep-1999 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
C:Accession: JCI106; A60490; 148243; S31439
R:Su, J.G.W.; Hsueh, A.J.W.
Biochem. Biophys. Res. Commun. 186, 293-300, 1992
A:Title: Characterization of mouse inhibin alpha gene and its promoter.
A:Reference number: JCI106; MUID:92337610; PMID:1632772
A:Accession: JCI106
A:Molecule type: DNA
A:Residues: 1-164,'R', 166-366 <SUG>
A:CROSS-references: GB:M95525; NID:q198404; PIDN:AAA39314.1; PID:q459875; GB:M95526
R:Tone, S.; Katoh, Y.; Fujimoto, H.; Togashi, S.; Yanazawa, M.; Kato, Y.; Higashinakagawa
Differentiation 44, 62-68, 1990
A:Title: Expression of inhibin alpha-subunit gene during mouse gametogenesis.
A:Reference number: A60490; MUID:91071531; PMID:2253839
A:Accession: A60490
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 49-366 <TUN>
A:CROSS-references: GB:X59597; NID:q296837; PIDN:CAA39424.1; PID:q296838
A:Experimental source: Swiss Webster
R:Albano, R.M.; Groome, N.; Smith, J.C.
Development 117, 711-723, 1993
A:Title: Activins are expressed in preimplantation mouse embryos and in ES and EC cells
A:Reference number: 148243; MUID:93321614; PMID:8330535
A:Accession: 148243
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-170,'V', 172-335,'T', 337-366 <ALB>
A:CROSS-references: EMBL:X69618; NID:q49936; PIDN:CAA49324.1; PID:q49937
C:Comment: This protein inhibits the secretion and synthesis of follicle-stimulating hor
C:Comment: this alpha chain is linked by two disulfide bonds to the beta-A chain in inh
C:Genetics:
A:Introns: 91/1
C:Superfamily: inhibin
C:Keywords: glycoprotein; gonad; heterodimer
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-233/Domain: propeptide #status predicted <PRO>
F:234-366/Product: inhibin alpha chain #status predicted <MAT>
F:147,269/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 97.9%; Score 140; DB 1; Length 366;
Best Local Similarity 96.0%; Pred. No. 2.2e-12;
Matches 24; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PWSPAALRLQLRPPEPSAHAFCHR 25
|||||
Db 241 PWSPAALRLQLRPPEPSAHAFCHR 265
|||||

RESULT 3
A25732
inhibin alpha chain precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A25732; S50897; A30161; A61548
R:Forage, R.G.; Ring, J.M.; Brown, R.W.; McInerney, B.V.; Cobon, G.S.; Gregson, R.P.; R
Proc. Natl. Acad. Sci. U.S.A. 83, 3091-3095, 1986
A:Title: Cloning and sequence analysis of cDNA species coding for the two subunits of in
A:Reference number: A94097; MUID:86205842; PMID:3458167
A:Accession: A25732
A:Molecule type: mRNA
A:Residues: 1-360 <FOR>
A:CROSS-references: GB:M13273; NID:q163194; PIDN:AAA97414.1; PID:q163195
A:Note: part of this sequence, including the amino end of the mature protein, was confir
R:Thompson, D.A.; Cronin, C.N.; Martin, F.
Eur. J. Biochem. 226, 751-764, 1994
A:Title: Genomic cloning and sequence analyses of the bovine alpha-, beta(A)- and beta(B
y DNase 1 footprinting.
A:Reference number: S50897; MUID:95112839; PMID:7813465
A:Accession: S50897
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-87 <THO>

A:CROSS-references: EMBL:U16237; NID:q563744; PIDN:AAB60262.1; PID:q563745
R:Sugino, K.; Nakamura, T.; Takio, K.; Iitani, K.; Miyamoto, K.; Hasegawa, Y.; Igara
Biochem. Biophys. Res. Commun. 159, 1323-1329, 1989
A:Title: Inhibin alpha-subunit monomer is present in bovine follicular fluid.
A:Reference number: A30161; MUID:89193729; PMID:2930562
A:Accession: A30161
A:Molecule type: protein
A:Residues: 18-37;227-246 <SUG>
R:Fukuda, M.; Miyamoto, K.; Hasegawa, Y.; Nomura, M.; Igarashi, M.; Kangawa, K.; Mat
Mol. Cell. Endocrinol. 44, 55-60, 1986
A:Title: Isolation of bovine follicular fluid inhibin of about 32 kDa.
A:Reference number: A61548; MUID:86136989; PMID:3081385
A:Accession: A61548
A:Molecule type: protein
A:Residues: 227-230 <FUK>
C:Comment: Inhibin suppresses follicle-stimulating hormone secretion.
C:Superfamily: inhibin
C:Keywords: disulfide bond; glycoprotein; gonad; heterodimer; hormone
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-226/Domain: propeptide #status predicted <PRO>
F:227-360/Product: inhibin alpha chain #status predicted <MAT>
F:140,262/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 91.6%; Score 131; DB 1; Length 360;
Best Local Similarity 92.0%; Pred. No. 4.3e-11;
Matches 23; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PWSPAALRLQLRPPEPSAHAFCHR 25
|||||
Db 234 PWSPAALRLQLRPPEPSAHAFCHR 258
|||||

RESULT 4
A24248
inhibin alpha chain precursor - human
C:Species: Homo sapiens (man)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Dec-2000
C:Accession: A23556; B25947; A24248
R:Stewart, A.G.; Milborrow, H.M.; Ring, J.M.; Crowther, C.E.; Forage, R.G.
FEBS Lett. 206, 329-334, 1986
A:Title: Human inhibin genes. Genomic characterisation and sequencing.
A:Reference number: A91366; MUID:87005283; PMID:3758355
A:Accession: A23556
A:Molecule type: DNA
A:Residues: 1-366 <STE>
A:CROSS-references: GB:X04445; NID:q43921; PIDN:CAA28040.1; PID:q1204105
R:Mayo, K.E.; Cerelli, G.M.; Spiess, J.; Rivier, J.; Rosenfeld, M.G.; Evans, R.M.; V
Proc. Natl. Acad. Sci. U.S.A. 83, 5849-5853, 1986
A:Title: Inhibin A-subunit cDNAs from porcine ovary and human placenta.
A:Reference number: A94116; MUID:86207450; PMID:4016724
A:Accession: B25947
A:Molecule type: mRNA
A:Residues: 1-366 <MAY>
A:CROSS-references: GB:M13981; NID:q186410; PIDN:AAA59166.1; PID:q307068
R:Mason, A.J.; Niall, H.D.; Seeburg, P.H.
Biochem. Biophys. Res. Commun. 135, 957-964, 1986
A:Title: Structure of two human ovarian inhibins.
A:Reference number: A90123; MUID:86186863; PMID:3754442
A:Accession: A24248
A:Molecule type: mRNA
A:Residues: 16,'V', 18,'S',20-366 <MAS>
A:CROSS-references: GB:M13144; NID:q186412; PIDN:AAA59167.1; PID:q186413
C:Comment: Activins A and B are homodimers of inhibin beta-A or inhibin beta-B, resp
bin beta-A and beta-B, respectively.
C:Genetics:
A:Gene: GDB:INHA
A:CROSS-references: GDB:120100; OMIM:147380
A:Map position: 2q33-2q36
A:Introns: 90/1
C:Superfamily: inhibin
C:Keywords: glycoprotein; gonad; heterodimer; hormone
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-232/Domain: propeptide #status predicted <PRO>

F:233-366/Product: inhibin alpha chain #status predicted <MAT>
 F:146,268,302/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 89.5%; Score 128; DB 1; Length 366;
 Best Local Similarity 88.0%; Pred. No. 1.2e-10;
 Matches 22; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PWSPALRLQLRPPEPSAHAFCHR 25
 |||||:|||||:|||||:|||||
 Db 240 PWSPALRLQLRPPEPSAHAFCHR 264

RESULT 5
 WFGCA
 Inhibin alpha chain precursor - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 18-Jun-1999
 C:Accession: A01392; A25947
 R:Masou, A.J.; Hayillick, J.S.; Ling, N.; Esch, F.; Ueno, N.; Ying, S.Y.; Guillemain, R.;
 Nature 318, 659-663, 1995
 A:Title: Complementary DNA sequences of ovarian follicular fluid inhibin show precursor
 A:Reference number: A93371; MUID:86092207; PMID:2417121
 A:Accession: A01392
 A:Molecule type: mRNA
 A:Residues: 1-364 <MAS>
 A:Cross-references: GB:X03265; NID:q1909; PIDN:CAA27019.1; PID:g2000
 R:Mayo, K.E.; Cerelli, G.M.; Spiess, J.; Rivier, J.; Rosenfeld, M.G.; Evans, R.M.; Vale,
 Proc. Natl. Acad. Sci. U.S.A. 83, 5849-5853, 1986
 A:Title: Inhibin A-subunit cDNAs from porcine ovary and human placenta.
 A:Reference number: A94116; MUID:86287350; PMID:3016724
 A:Accession: A25947
 A:Molecule type: mRNA
 A:Residues: 1-119, R', 121-124, A', 126-364 <MAY>
 A:Cross-references: GB:M13980; NID:q164518; PIDN:AAA31057.1; PID:g164519
 C:Comment: The mature protein is the carboxyl-terminal segment of a precursor polypeptide
 identical forms of inhibin have been isolated (A and B) that differ in the amino-terminal
 C:Comment: Inhibin is secreted by ovaries or testes and inhibits the secretion of follicle
 C:Superfamily: inhibin
 C:Keywords: contraceptive; follitropin inhibitor; glycoprotein; gonad
 F:1-17/Domain: signal sequence #status predicted <SIG>
 F:18-230/Domain: propeptide #status predicted <PRO>
 F:231-364/Product: inhibin alpha chain #status predicted <MAT>
 F:144,266/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 88.8%; Score 127; DB 1; Length 364;
 Best Local Similarity 88.0%; Pred. No. 1.6e-10;
 Matches 22; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 PWSPALRLQLRPPEPSAHAFCHR 25
 |||||:|||||:|||||:|||||
 Db 238 PWSPALRLQLRPPEPSAHAFCHR 262

RESULT 6
 IS1215
 Inhibin alpha-subunit precursor - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 17-Mar-2000
 C:Accession: IS1215
 R:Wang, S.Y.; Johnson, P.A.
 Biol. Reprod. 49, 453-458, 1993
 A:Title: Complementary deoxyribonucleic acid cloning and sequence analysis of the alpha-
 A:Reference number: IS1215; MUID:94002740; PMID:8399835
 A:Accession: IS1215
 A:Status: preliminary;
 A:Molecule type: mRNA
 A:Residues: 1-328 <WAN>
 A:Cross-references: GB:S65963; NID:q430815; PID:g430816
 C:Superfamily: inhibin

Query Match 62.2%; Score 89; DB 2; Length 328;
 Best Local Similarity 64.0%; Pred. No. 4e-05;
 Matches 16; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 PWSPALRLQLRPPEPSAHAFCHR 25
 |||||:|||||:|||||:|||||
 Db 219 PWSGALSLLQRPSEDVAATHCKR 243

RESULT 7
 A57788
 enoyl-[acyl-carrier-protein] reductase (NADPH2, B-specific) (EC 1.3.1.10) (version
 N:Contains: 3-hydroxypalmitoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.61); 3-
 oyl-[acyl-carrier-protein] reductase (NADPH, B-specific) (EC 1.3.1.10); oleoyl-[acy-
 protein] S-malonyltransferase (EC 2.3.1.39)
 C:Species: Homo sapiens (man)
 C:Date: 23-Feb-1996 #sequence_revision 10-Jul-1998 #text_change 03-Jun-2002
 C:Accession: A57788; B57788
 R:Jayakumar, A.; Tai, M.H.; Huang, W.Y.; al-Peei, W.; Hsu, M.; Abu-Elheiga, L.; Chi
 Proc. Natl. Acad. Sci. U.S.A. 92, 8695-8699, 1995
 A:Title: Human fatty acid synthase: properties and molecular cloning.
 A:Reference number: A57788; MUID:96004605; PMID:7567999
 A:Accession: A57788
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-2504 <JAY1>
 A:Cross-references: EMBL:U26644; NID:q1049052; PIDN:AA50259.1; PID:q1049053
 A:Accession: B57788
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1297, 1PTQVASSLSLSVQOVA, 1316-2504 <JAY2>
 C:Genetics:
 A:Gene: GDB:FASN
 A:Cross-references: GDB:342064; OMIM:600212
 A:Map position: 17q25-17q25
 C:Superfamily: rat fatty-acid synthase; 3-oxoacyl-[acyl-carrier-protein] synthase 1
 ydrase homology; short-chain alcohol dehydrogenase homology; [acyl-carrier-prote-
 C:Keywords: acyltransferase; carbon-oxygen lyase; carrier protein; coenzyme A; fatty
 lyase
 F:22-403/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>
 F:492-773/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT>
 F:1315-1333/Region: catalytic (of 3-hydroxypalmitoyl-[acyl-carrier-protein] dehydra
 F:1545-1849/Domain: long-chain alcohol dehydrogenase homology <LADH>
 F:1664-1694/Region: beta-alpha-beta NADP nucleotide-binding fold
 F:1879-2061/Domain: short-chain alcohol dehydrogenase homology <SADH>
 F:2116-2,867/Domain: acyl carrier protein homology <ACP>
 F:2212-2504/Domain: oleoyl-[acyl-carrier-protein] hydrolase #status predicted <ENZ7
 F:2228-2480/Domain: oleoyl-[acyl-carrier-protein] hydrolase homology <ACPH>
 F:161/Active site: Cys (of 3-oxoacyl-l-acyl-carrier-protein) synthase) #status predi
 F:580/Active site: Ser (covalent substrate-binding) (of [acyl-carrier-protein] S-ma
 F:1696,1699/Active site: Ser, lys (of enoyl-[acyl-carrier-protein] reductase) #stat
 F:1921/Active site: lys (of 3-oxoacyl-[acyl-carrier-protein] reductase) #status pre
 F:2151/Binding site: phosphatidylserine (Ser) (covalent) #status predicted
 F:2302/Active site: Ser (of oleoyl-[acyl-carrier-protein] hydrolase) #status predic

Query Match 37.8%; Score 54; DB 1; Length 2504;
 Best Local Similarity 71.4%; Pred. No. 35;
 Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 9 LLORPEEPSAHAF 22
 ||:|||||:
 Db 1514 LLEDKPEEPTAHAF 1527

RESULT 8
 UBHUG
 tubulin gamma chain - human
 C:Species: Homo sapiens (man)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 22-Jun-1999
 C:Accession: A39527
 R:Zheng, Y.; Jung, M.K.; Oakley, B.R.
 Cell 65, 817-823, 1991
 A:Title: Gamma-tubulin is present in Drosophila melanogaster and Homo sapiens and i
 A:Reference number: A39527; MUID:91249388; PMID:1904010
 A:Accession: A39527
 A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA
 A:Residues: 1-451 <2HE>
 A:Cross-references: GB:M61764; NID:g183702; PIDN:AAA52620.1; PID:g183703
 C:Comment: This protein is a component of the centrosome that may play a role in microtubule binding.
 C:Genetics:
 A:Gene: GDB:TUBG
 A:Cross-references: GDB:128500; OMIM:191135
 A:Map position: 13q13-13q14.1
 C:Superfamily: tubulin
 C:Keywords: GTP binding; microtubule

Query Match 35.7%; Score 51; DB 1; Length 451;
 Best Local Similarity 45.5%; Pred. No. 15;
 Matches 10; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

QY 1 PWSAALR--LLQRPPEPSAH 20
 II IIIII I : I IIII
 DB 350 PWGPASTQVALSKSPYLPFAH 371

RESULT 9

UBXLG

tubulin gamma chain - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 22-Jun-1999
 C:Accession: A39528
 R:Stearns, J.; Evans, L.; Kirschner, M.
 Cell 65, 825-836, 1991

A:Title: Gamma-tubulin is a highly conserved component of the centrosome.
 A:Reference number: A39528; MUID:91249389; PMID:1840506
 A:Accession: A39528

A>Status: nucleic acid sequence not shown
 A:Molecule type: mRNA

A:Residues: 1-451 <STE>

A:Cross-references: GB:M63446; NID:g214164; PIDN:AAA49720.1; PID:g214165

C:Comment: This protein is a component of the centrosome that may play a role in microtubule binding.
 C:Genetics:
 A:Gene: Xgam
 C:Superfamily: tubulin
 C:Keywords: GTP binding; microtubule

Query Match 35.7%; Score 51; DB 1; Length 451;
 Best Local Similarity 45.5%; Pred. No. 15;
 Matches 10; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

QY 1 PWSAALR--LLQRPPEPSAH 20
 II IIIII I : I IIII
 DB 350 PWGPASTQVALSKSPYLPFAH 371

RESULT 10

E83800

hypothetical protein bhl205 [imported] - Bacillus halodurans (strain C-125)

C:Species: Bacillus halodurans
 C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
 C:Accession: E83800

R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, N.; Fujii, F.; Hirai

Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
 A:Reference number: A83650; MUID:20512582; PMID:11058132

A:Accession: E83800

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-365 <STO>

A:Cross-references: GB:AP001511; GB:BA000004; NID:g10173727; PIDN:BA004924.1; GSPDB:GN00
 A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: BHL205

Query Match 34.3%; Score 49; DB 2; Length 365;
 Best Local Similarity 61.1%; Pred. No. 24;
 Matches 11; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 WSPAALRLQLQRPPEPSA 19
 II IIIII I I
 DB 324 WSGGLRLQLQRCESAGA 341

RESULT 11

T44497

hypothetical protein [imported] - Thermomonospora fusca

C:Species: Thermomonospora fusca
 C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000

C:Accession: T44497

R:Irwin, D.I.; Zhang, S.; Wilson, D.B.

submitted to the EMBL Data Library, April 1999

A:Description: Characterization of a Thermomonospora fusca family 48 exocellulase E

A:Reference number: Z22783

A:Accession: T44497

A>Status: preliminary; translated from GB/EMBL/UDBJ

A:Molecule type: DNA

A:Residues: 1-128 <IRW>

A:Cross-references: EMBL:AF144563; PIDN:AA039948.1

A:Experimental source: strain YX

Query Match 33.6%; Score 48; DB 2; Length 128;
 Best Local Similarity 47.1%; Pred. No. 11;
 Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 4 PAALRLQLQRPPEPSAH 20
 II IIII I : I I I
 DB 18 PAGPHITQLRHPQAAH 34

RESULT 12

T09236

nifZ protein - Frankia alni

C:Species: Frankia alni

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T09236

R:Benson, D.R.

submitted to the EMBL Data Library, November 1998

A:Reference number: Z16624

A:Accession: T09236

A>Status: translated from GB/EMBL/UDBJ

A:Molecule type: DNA

A:Residues: 1-192 <BEN>

A:Cross-references: EMBL:129299; NID:g3953454; PID:g497435

A:Experimental source: strain cp11

C:Genetics:

A:Gene: nifZ

C:Keywords: nitrogen fixation

Query Match 33.5%; Score 48; DB 2; Length 192;
 Best Local Similarity 44.4%; Pred. No. 17;
 Matches 8; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 3 SPAALRLQLQRPPEPSAH 20
 IIII : : I IIII
 DB 102 APAALVLAERKVPAPAAH 119

RESULT 13

JC4207

nitrogenase NifZ chain - Frankia sp.

N:Alternate names: NifZ protein

C:Species: Frankia sp.

C:Date: 10-Sep-1995 #sequence_revision 27-Oct-1995 #text_change 22-Oct-1999

C:Accession: JC4207

R:Harriott, O.T.; Hosted, T.J.; Benson, D.R.

Gene 161, 63-67, 1995

A:Title: Sequences of nifX, nifW, nifZ, nifB and two ORF in the Frankia nitrogen fix

A:Reference number: JC4203; MUID:95369734; PMID:7642138

A:Accession: JC4207

A:Molecule type: DNA

A:Residues: 1-192 <HAR>

A:Cross-references: GB:L29299; NID:g497430; PIDN:AAC82974.1; PID:g497435
 C:Comment: This protein has an Ala and Pro rich region at its carboxyl-terminal region.
 C:Genetics:
 A:Gene: nifZ
 C:Keywords: nitrogen fixation

Query Match 33.6%; Score 48; DB 2; Length 192;
 Best Local Similarity 44.4%; Pred. No. 17;
 Matches 8; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 3 SPAALRLIQRPPPSAH 20
 :||| : : : ||||
 Db 102 APAAVLVAEKVPAEPAAH 119

RESULT 14

A49361
 peripheral benzodiazepine receptor-related protein - human
 C:Species: Homo sapiens (man)
 C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 05-Nov-1999
 C:Accession: A49361
 R:Lin, D.; Chang, Y.J.; Strauss, J.F.; Miller, W.L.
 Genomics 18, 643-650, 1993
 A:Title: The human peripheral benzodiazepine receptor gene: cloning and characterization
 A:Reference number: A49361; MUID:94140364; PMID:8307574
 A:Accession: A49361
 A>Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-102 <RES>
 A:Cross-references: GB:L21950; NID:g483401; PIDN:AAA18227.1; PID:g488420

Query Match 32.9%; Score 47; DB 2; Length 102;
 Best Local Similarity 39.1%; Pred. No. 12;
 Matches 9; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 2 WSPAALRLIQRPPPEPSAHAFCH 24
 :||| : || : || : ||
 Db 59 WCTAARVSAHPTDCSTSRCH 91

RESULT 15

H87577
 nitroreductase family protein [imported] - Caulobacter crescentus
 C:Species: Caulobacter crescentus
 C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 03-Jun-2002
 C:Accession: H87577
 R:Kierman, W.C.; Feidblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
 B.; Taub, M.T.; DeBoy, R.T.; Dodson, R.J.; DuKin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A:Title: Complete Genome Sequence of Caulobacter crescentus.
 A:Reference number: H87249; MUID:21173698; PMID:11259647
 A:Accession: H87577
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-181 <STO>
 A:Cross-references: GB:AE005673; NID:g13424234; PIDN:AAK24620.1; GSPDB:GN00148
 C:Genetics:
 A:Gene: CC2653
 C:Superfamily: Methanobacterium thermoautotrophicum NADPH-oxidoreductase

Query Match 32.9%; Score 47; DB 2; Length 181;
 Best Local Similarity 33.3%; Pred. No. 22;
 Matches 13; Conservative 2; Mismatches 6; Indels 18; Gaps 1;

QY 5 AALRLIQRPP-----EPPSAHAFCHR 25
 :||| : ||| : || : |||
 Db 76 AALRLIQRPPVAVISRIIPGEIPEWEQROSASAVCHQ 114

Search completed: March 13, 2003, 13:59:34
 Job time : 21.5 secs